Figure 1

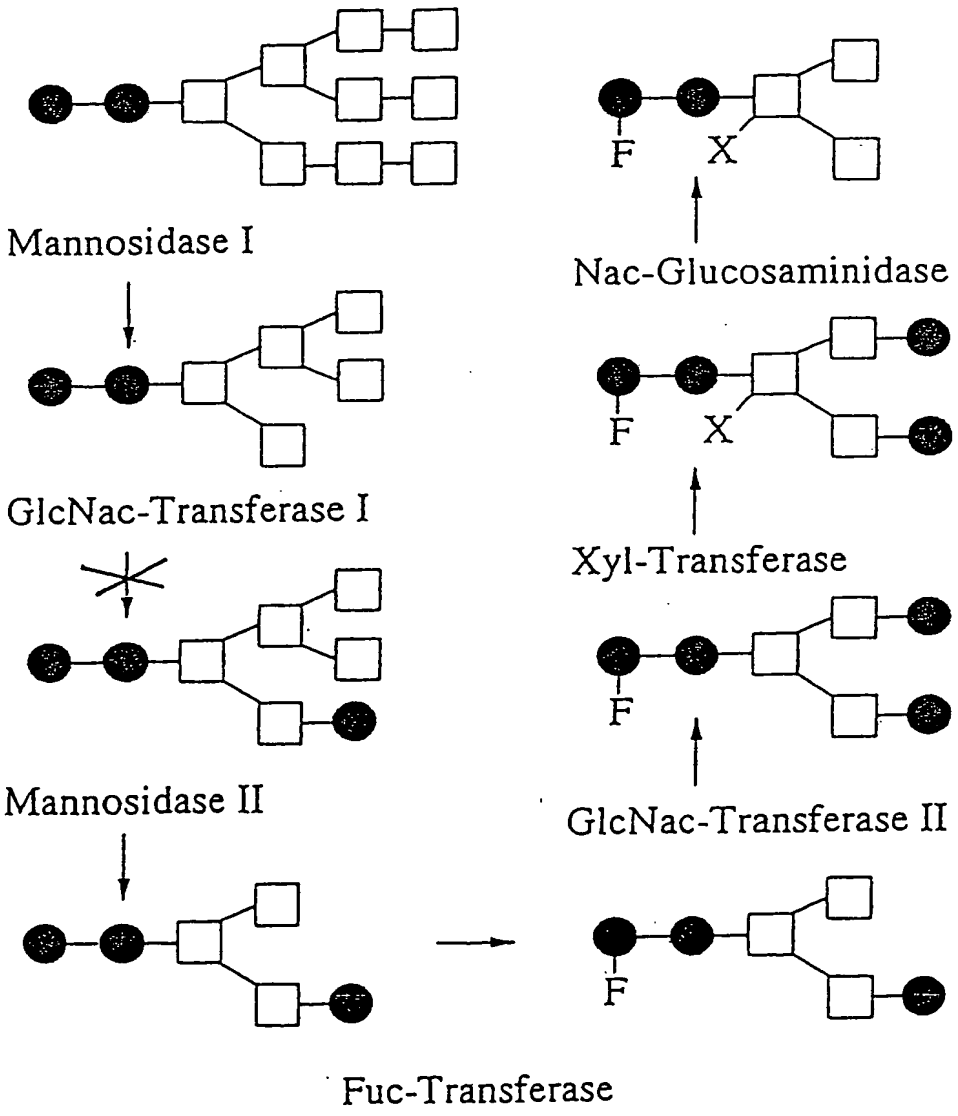
Mannosidase I
GlcNac-Transferase I
Mannosidase II
Fuc-Transferase
Nac-Glucosaminidase
Xyl-Transferase
GlcNac-Transferase II
F
X

Figure 2

A1 *GntI* cDNA

```
GAATTCGCGG CCGCCTGAGA AACCCTCGAA TTCAATTTCG CATTTGGCAG AG ATG          55
                                                           Met
                                                            1

AGA GGG AAC AAG TTT TGC TTT GAT TTA CGG TAC CTT CTC GTC GTG GCT        103
Arg Gly Asn Lys Phe Cys Phe Asp Leu Arg Tyr Leu Leu Val Val Ala
                5                  10                  15

GCT CTC GCC TTC ATC TAC ATA CAG ATG CGG CTT TTC GCG ACA CAG TCA        151
Ala Leu Ala Phe Ile Tyr Ile Gln Met Arg Leu Phe Ala Thr Gln Ser
            20                  25                  30

GAA TAT GTA GAC CGC CTT GCT GCT GCA ATT GAA GCA GAA AAT CAT TGT        199
Glu Tyr Val Asp Arg Leu Ala Ala Ala Ile Glu Ala Glu Asn His Cys
        35                  40                  45

ACA AGT CAG ACC AGA TTG CTT ATT GAC AAG ATT AGC CAG CAG CAA GGA        247
Thr Ser Gln Thr Arg Leu Leu Ile Asp Lys Ile Ser Gln Gln Gln Gly
    50                  55                  60                  65

AGA GTA GTA GCT CTT GAA GAA CAA ATG AAG CAT CAG GAC CAG GAG TGC        295
Arg Val Val Ala Leu Glu Glu Gln Met Lys His Gln Asp Gln Glu Cys
                70                  ↑   75                  80

CGG CAA TTA AGG GCT CTT GTT CAG GAT CTT GAA AGT AAG GGC ATA AAA        343
Arg Gln Leu Arg Ala Leu Val Gln Asp Leu Glu Ser Lys Gly Ile Lys
            85                  90                  95

AAG TTA ATC GGA GAT GTG CAG ATG CCA GTG GCA GCT GTA GTT GTT ATG        391
Lys Leu Ile Gly Asp Val Gln Met Pro Val Ala Ala Val Val Val Met
        100                 105                 110

GCT TGC AGT CGT ACT GAC TAC CTG GAG AGG ACT ATT AAA TCC ATC TTA        439
Ala Cys Ser Arg Thr Asp Tyr Leu Glu Arg Thr Ile Lys Ser Ile Leu
    115                 120                 125

AAA TAC CAA ACA TCT GTT GCA TCA AAA TAT CCT CTT TTC ATA TCC CAG        487
Lys Tyr Gln Thr Ser Val Ala Ser Lys Tyr Pro Leu Phe Ile Ser Gln
130                 135                 140                 145

GAT GGA TCA AAT CCT GAT GTA AGA AAG CTT GCT TTG AGC TAT GGT CAG        535
Asp Gly Ser Asn Pro Asp Val Arg Lys Leu Ala Leu Ser Tyr Gly Gln
                150                 155                 160

CTG ACG TAT ATG CAG CAC TTG GAT TAT GAA CCT GTG CAT ACT GAA AGA        583
Leu Thr Tyr Met Gln His Leu Asp Tyr Glu Pro Val His Thr Glu Arg
            165                 170                 175

CCA GGG GAA CTG GTT GCA TAC TAC AAG ATT GCA CGT CAT TAC AAG TGG        631
Pro Gly Glu Leu Val Ala Tyr Tyr Lys Ile Ala Arg His Tyr Lys Trp
        180                 185                 190

GCA TTG GAT CAG CTG TTT CAC AAG CAT AAT TTT AGC CGT GTT ATC ATA        679
Ala Leu Asp Gln Leu Phe His Lys His Asn Phe Ser Arg Val Ile Ile
    195                 200             *   205

CTA GAA GAT GAT ATG GAA ATT GCT GCT GAT TTT TTT GAC TAT TTT GAG        727
Leu Glu Asp Asp Met Glu Ile Ala Ala Asp Phe Phe Asp Tyr Phe Glu
210                 215                 220                 225
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Figure 2 (continued)

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GCT GGA GCT ACT CTT CTT GAC AGA GAC AAG TCG ATT ATG GCT ATT TCT          775
Ala Gly Ala Thr Leu Leu Asp Arg Asp Lys Ser Ile Met Ala Ile Ser
                230                 235                 240

TCT TGG AAT GAC AAT GGA CAA AGG CAG TTC GTC CAA GAT CCT GAT GCT          823
Ser Trp Asn Asp Asn Gly Gln Arg Gln Phe Val Gln Asp Pro Asp Ala
            245                 250                 255

CTT TAC CGC TCA GAC TTT TTT CCT GGT CTT GGA TGG ATG CTT TCA AAA          871
Leu Tyr Arg Ser Asp Phe Phe Pro Gly Leu Gly Trp Met Leu Ser Lys
        260                 265                 270

TCA ACT TGG TCC GAA CTA TCT CCA AAG TGG CCA AAG GCT TAC TGG GAT          919
Ser Thr Trp Ser Glu Leu Ser Pro Lys Trp Pro Lys Ala Tyr Trp Asp
    275                 280                 285

GAC TGG CTA AGG CTG AAA GAA AAT CAC AGA GGT CGA CAA TTT ATT CGC          967
Asp Trp Leu Arg Leu Lys Glu Asn His Arg Gly Arg Gln Phe Ile Arg
290                 295                 300                 305

CCA GAA GTT TGC AGA ACG TAC AAT TTT GGT GAG CAT GGT TCT AGT TTG         1015
Pro Glu Val Cys Arg Thr Tyr Asn Phe Gly Glu His Gly Ser Ser Leu
                310                 315                 320

GGG CAG TTT TTT AAG CAG TAT CTT GAG CCA ATT AAG CTA AAT GAT GTC         1063
Gly Gln Phe Phe Lys Gln Tyr Leu Glu Pro Ile Lys Leu Asn Asp Val
            325                 330                 335

CAG GTT GAT TGG AAG TCA ATG GAC CTA AGT TAC CTT TTG GAG GAC AAC         1111
Gln Val Asp Trp Lys Ser Met Asp Leu Ser Tyr Leu Leu Glu Asp Asn
        340                 345                 350

TAT GTG AAA CAC TTT GGC GAC TTG GTT AAA AAG GCT AAG CCC ATC CAC         1159
Tyr Val Lys His Phe Gly Asp Leu Val Lys Lys Ala Lys Pro Ile His
    355                 360                 365

GGA GCT GAT GCT GTT TTG AAA GCA TTT AAC ATA GAT GGT GAT GTG CGT         1207
Gly Ala Asp Ala Val Leu Lys Ala Phe Asn Ile Asp Gly Asp Val Arg
370                 375                 380                 385

ATT CAG TAC AGA GAC CAA CTA GAC TTT GAA GAT ATC GCT CGA CAG TTT         1255
Ile Gln Tyr Arg Asp Gln Leu Asp Phe Glu Asp Ile Ala Arg Gln Phe
                390                 395                 400

GGC ATT TTT GAA GAA TGG AAG GAT GGT GTA CCA CGG GCA GCA TAT AAA         1303
Gly Ile Phe Glu Glu Trp Lys Asp Gly Val Pro Arg Ala Ala Tyr Lys
            405                 410                 415

GGG ATA GTA GTT TTC CGG TTT CAA ACA TCT AGA CGT GTG TTC CTT GTT         1351
Gly Ile Val Val Phe Arg Phe Gln Thr Ser Arg Arg Val Phe Leu Val
        420                 425                 430

TCC CCT GAT TCT CTT CGA CAA CTT GGA GTT GAA GAT ACT TAG                 1393
Ser Pro Asp Ser Leu Arg Gln Leu Gly Val Glu Asp Thr End
    435                 440                 445

CGAAGATATG ATTGGAGCCT GAGCAACAAT TTAGACTTAT TTGGTAGGAT ACATTTGAAA      1453

GAGCTGACAC GAAAAGTATG ACTACCAGTA GCTACATGCA ACATTTTAAT GTTAATGGAA      1513

GGAACCCACT GCTTATTGTT GGAATGGATG AATCATCACC ACATCCTATT ATTCAAGTTT      1573

ACAAACATAA AGAGGAAATG TTGCCCTATA AAAACAAATT TTTTGTTTCT AAGAAGGAAC      1633

GTTACGATTA TGAGCAACTT TGGCGGCCGC GAATTC                                 1669
```

Figure 3A

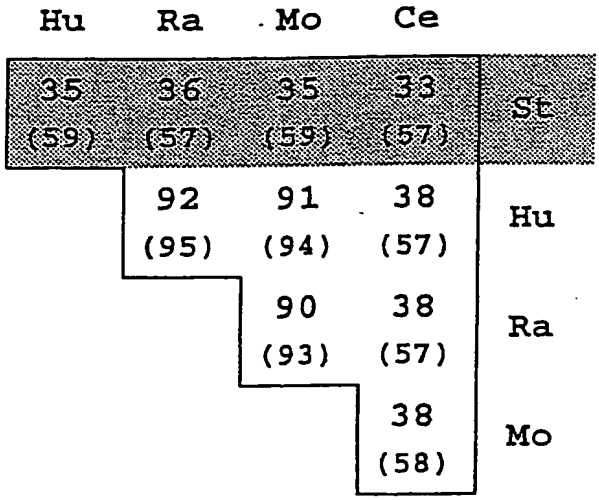

Figure 3B

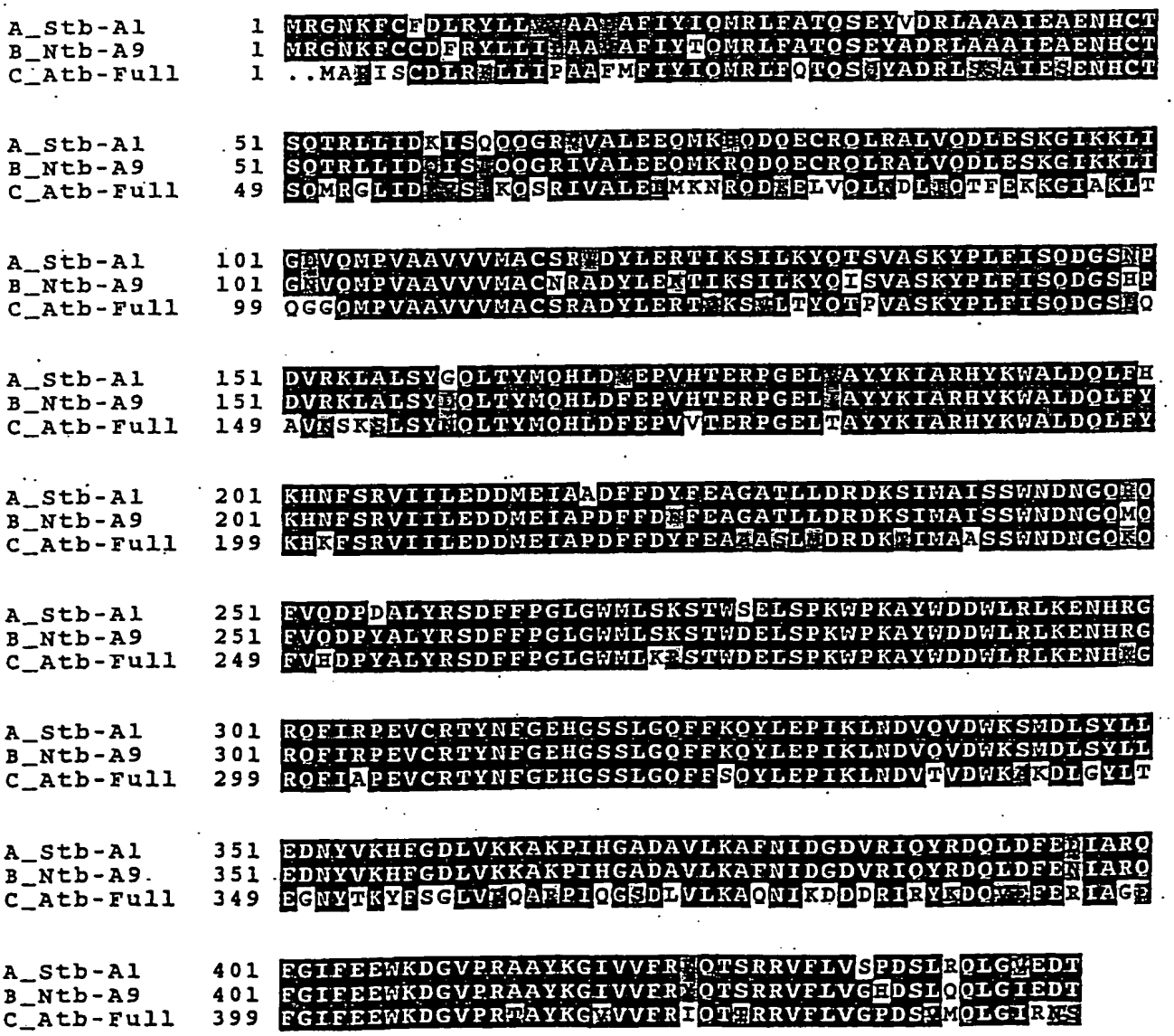

Figure 4

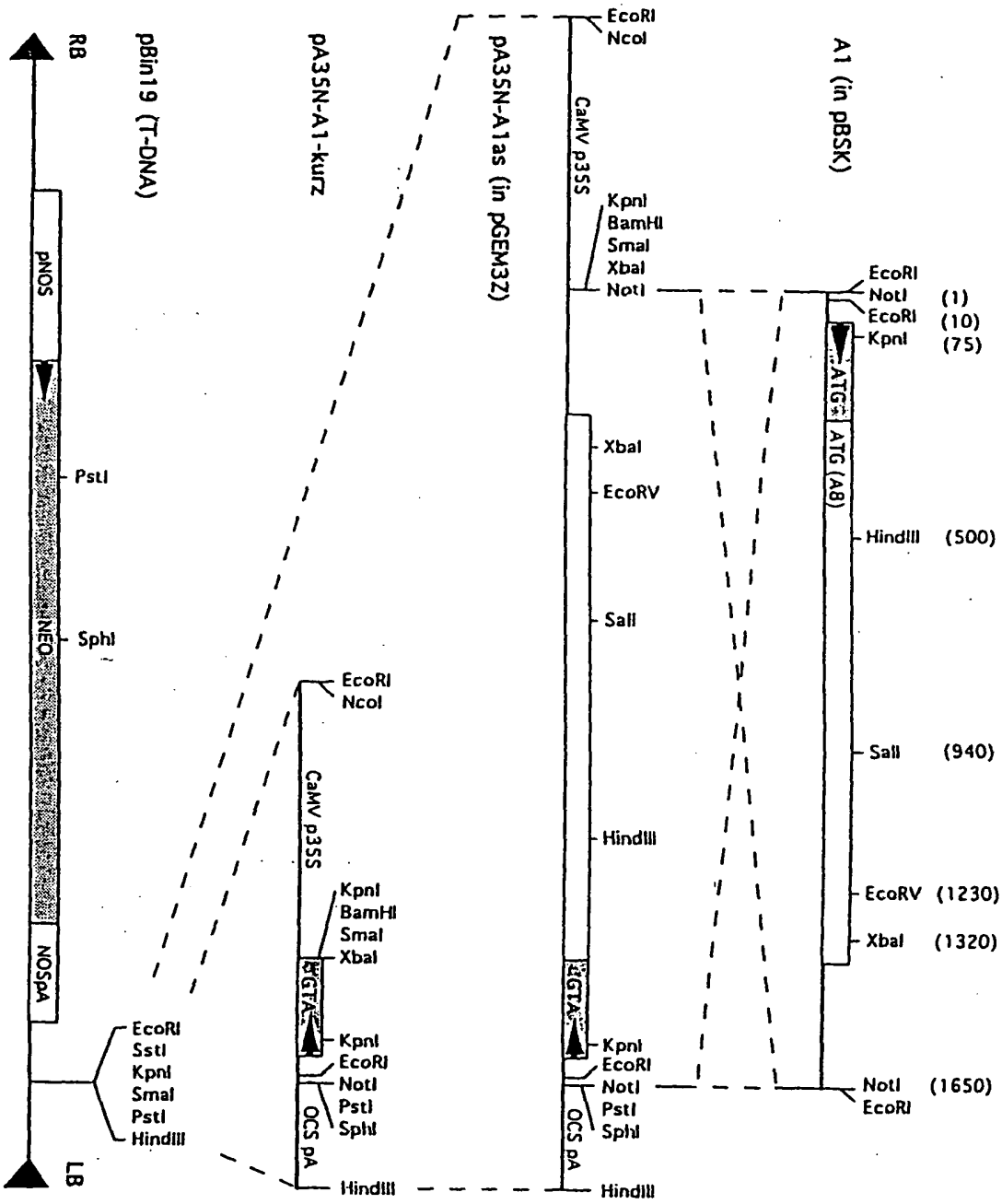
pBin19 (T-DNA)
RB
LB
pNOS
NEO
NOSpA
PstI
SphI
EcoRI
SstI
KpnI
SmaI
PstI
HindIII
pA35N-A1-kurz
EcoRI
NcoI
CaMV p35S
KpnI
BamHI
SmaI
XbaI
A'GTA
KpnI
EcoRI
NotI
PstI
SphI
OCS pA
HindIII
pA35N-A1as (in pGEM3Z)
EcoRI
NcoI
CaMV p35S
KpnI
BamHI
SmaI
XbaI
NotI
XbaI
EcoRV
SalI
HindIII
A'GTA
KpnI
EcoRI
NotI
PstI
SphI
OCS pA
HindIII
A1 (in pBSK)
EcoRI
NotI (1)
EcoRI (10)
KpnI (75)
ATG
ATG (A8)
HindIII (500)
SalI (940)
EcoRV (1230)
XbaI (1320)
NotI (1650)
EcoRI

Figure 5

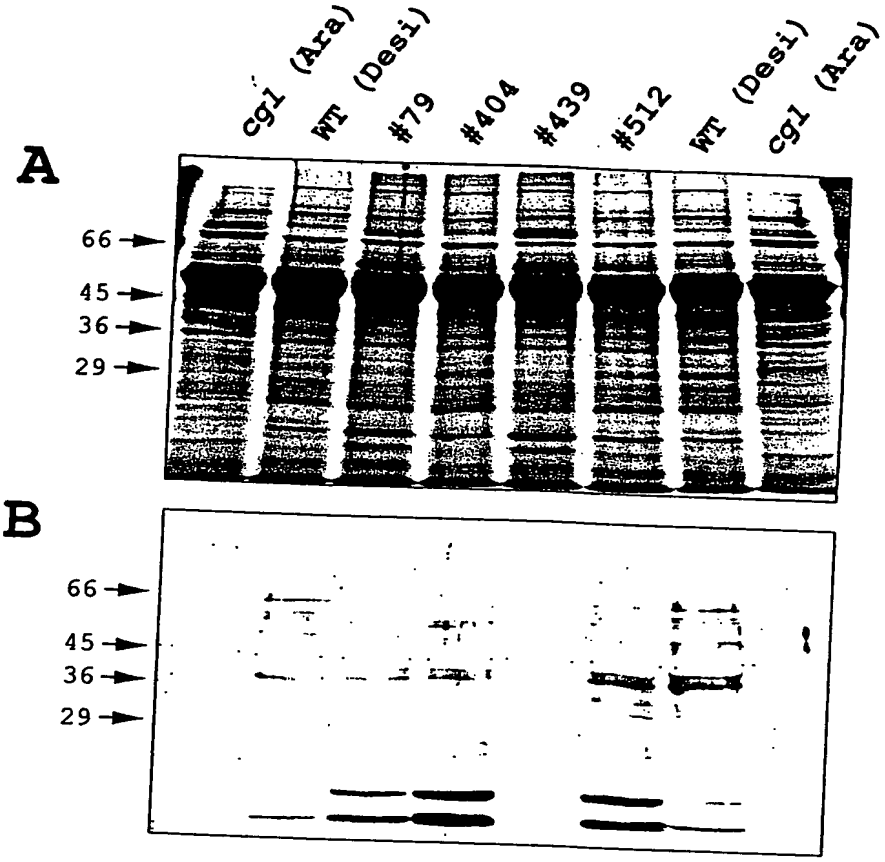

Figure 6